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NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Dec 17	The CA Lexicon available in the CAPLUS and CA files
NEWS 3	Feb 06	Engineering Information Encompass files have new names
NEWS 4	Feb 16	TOXLINE no longer being updated
NEWS 5	Apr 23	Search Derwent WPINDEX by chemical structure
NEWS 6	Apr 23	PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
NEWS 7	May 07	DGENE Reload
NEWS 8	Jun 20	Published patent applications (A1) are now in USPATFULL
NEWS 9	JUL 13	New SDI alert frequency now available in Derwent's DWPI and DPCI
NEWS 10	Aug 23	In-process records and more frequent updates now in MEDLINE
NEWS 11	Aug 23	PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
NEWS 12	Aug 23	Adis Newsletters (ADISNEWS) now available on STN
NEWS 13	Sep 17	IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH
NEWS 14	Oct 09	Korean abstracts now included in Derwent World Patents Index
NEWS 15	Oct 09	Number of Derwent World Patents Index updates increased
NEWS 16	Oct 15	Calculated properties now in the REGISTRY/ZREGISTRY File
NEWS 17	Oct 22	Over 1 million reactions added to CASREACT
NEWS 18	Oct 22	DGENE GETSIM has been improved
NEWS 19	Oct 29	AAASD no longer available
NEWS 20	Nov 19	New Search Capabilities USPATFULL and USPAT2
NEWS 21	Nov 19	TOXCENTER(SM) - new toxicology file now available on STN
NEWS 22	Nov 29	COPPERLIT now available on STN
NEWS 23	Nov 29	DWPI revisions to NTIS and US Provisional Numbers
NEWS 24	Nov 30	Files VETU and VETB to have open access
NEWS 25	Dec 10	WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
NEWS 26	Dec 10	DGENE BLAST Homology Search
NEWS 27	Dec 17	WELDASEARCH now available on STN
NEWS 28	Dec 17	STANDARDS now available on STN
NEWS 29	Dec 17	New fields for DPCI
NEWS 30	Dec 19	CAS Roles modified
NEWS 31	Dec 19	1907-1946 data and page images added to CA and CAplus

NEWS EXPRESS	August 15 CURRENT WINDOWS VERSION IS V6.0c, CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP), AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
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NEWS INTER	General Internet Information
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FILE 'HOME' ENTERED AT 08:25:42 ON 09 JAN 2002

=> file medline, biosis, caplus, embase, scisearch
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FULL ESTIMATED COST 0.30 0.30

FILE 'MEDLINE' ENTERED AT 08:26:35 ON 09 JAN 2002

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=> s C(a)elegans(p)genom(a)library
(A)LIBRARY IS NOT A RECOGNIZED COMMAND
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=> s C(a) elegans(p)genom?(a)libr?
L1 59 C(A) ELEGANS(P) GENOM?(A) LIBR?

=> s C(a) elegans(p)genom?(a)library(p)pheno?
L2 11 C(A) ELEGANS(P) GENOM?(A) LIBRARY(P) PHENO?

=> display total ibib abs L2

L2 ANSWER 1 OF 11 MEDLINE
ACCESSION NUMBER: 1999234093 MEDLINE
DOCUMENT NUMBER: 99234093 PubMed ID: 10216251
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in Caenorhabditis briggsae.
AUTHOR: Vatcher G P; Barbazuk W B; O'Neil N J; Marra M A; Ha T; Baillie D L
CORPORATE SOURCE: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, Canada.
SOURCE: GENE, (1999 Apr 16) 230 (2) 137-44.
Journal code: FOP; 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199906
ENTRY DATE: Entered STN: 19990614
Last Updated on STN: 19990614

Entered Medline: 19990601

AB In the nematode Caenorhabditis elegans, the maternal effect lethal gene mel-32 encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, mel-32(SHMT) genomic DNA from **C. elegans** was used to screen a **genomic library** from the closely related nematode Caenorhabditis briggsae. The C. briggsae genomic clone identified fully rescues the Mel-32 **phenotype** in **C. elegans**, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the mel-32(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 2 OF 11 MEDLINE
ACCESSION NUMBER: 96234073 MEDLINE
DOCUMENT NUMBER: 96234073 PubMed ID: 8650202
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from Kluyveromyces lactis.
AUTHOR: Abeijon C; Robbins P W; Hirschberg C B
CORPORATE SOURCE: Department of Biochemistry and Molecular Biology, University of Massachusetts Medical Center, Worcester, 01655, USA.
CONTRACT NUMBER: GM 30365 (NIGMS)
GM 45188 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Jun 11) 93 (12) 5963-8. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U48413
ENTRY MONTH: 199607
ENTRY DATE: Entered STN: 19960805
Last Updated on STN: 19960805
Entered Medline: 19960725

AB The mannan chains of Kluyveromyces lactis mannoproteins are similar to those of Saccharomyces cerevisiae except that they lack mannose phosphate and have terminal alpha1-->2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to S. cerevisiae. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of K. lactis, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the K. lactis Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type K. lactis in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein

of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from S. cerevisiae and **C. elegans**. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of K. lactis.

L2 ANSWER 3 OF 11 BIOSIS COPYRIGHT 2002 BIOSIS
ACCESSION NUMBER: 1999:248195 BIOSIS
DOCUMENT NUMBER: PREV199900248195
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in Caenorhabditis briggsae.
AUTHOR(S): Vatcher, G. P.; Barbazuk, W. B.; O'Neil, N. J.; Marra, M. A.; Ha, T.; Baillie, D. L. (1)
CORPORATE SOURCE: (1) Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, British Columbia, V5A 1S6 Canada
SOURCE: Gene (Amsterdam), (April 16, 1999) Vol. 230, No. 2, pp. 137-144.
ISSN: 0378-1119.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB In the nematode Caenorhabditis elegans, the maternal effect lethal gene mel-32 encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, mel-32(SHMT) genomic DNA from **C. elegans** was used to screen a **genomic library** from the closely related nematode Caenorhabditis briggsae. The C. briggsae genomic clone identified fully rescues the Mel-32 **phenotype** in **C. elegans**, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the mel-32(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 4 OF 11 BIOSIS COPYRIGHT 2002 BIOSIS
ACCESSION NUMBER: 1996:332779 BIOSIS
DOCUMENT NUMBER: PREV199699055135
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from Kluyveromyces lactis.
AUTHOR(S): Abeijon, Claudia (1); Robbins, Phillips W.; Hirschbeg, Carlos B. (1)
CORPORATE SOURCE: (1) Dep. Biochem.. Mol. Biol., Univ. Mass. Med. Cent., Worcester, MA 01655 USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) Vol. 93, No. 12, pp. 5963-5968.
ISSN: 0027-8424.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The mannan chains of Kluyveromyces lactis mannoproteins are similar to those of Saccharomyces cerevisiae except that they lack mannose phosphate and have terminal alpha-1 fwdarw 2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to S. cerevisiae. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant

of K. lactis, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the K. lactis Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type K. lactis in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from S. cerevisiae and **C. elegans**. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of K. lactis.

L2 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:35000 CAPLUS
DOCUMENT NUMBER: 132:103727
TITLE: Characterization of gene function using double-stranded RNA inhibition
INVENTOR(S): Plaetinck, Geert; Platteeuw, Christ; Mortier, Katherine; Bogaert, Thierry
PATENT ASSIGNEE(S): Devgen N.V., Belg.
SOURCE: PCT Int. Appl., 97 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000001846	A2	20000113	WO 1999-EP4718	19990702
WO 2000001846	A3	20000615		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9949079	A1	20000124	AU 1999-49079	19990702
GB 2349885	A1	20001115	GB 2000-20485	19990702
EP 1093526	A2	20010425	EP 1999-932836	19990702
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
GB 2362885	A1	20011205	GB 2001-18514	19990702
NO 2001000019	A	20010305	NO 2001-19	20010102

PRIORITY APPLN. INFO.:

GB 1998-14536	A	19980703
GB 1998-27152	A	19981209
GB 2000-20485	A3	19990702
WO 1999-EP4718	W	19990702

AB There is provided a method of identifying DNA responsible for conferring a particular **phenotype** in a cell which method comprises (a) constructing a cDNA or **genomic library** of the DNA of

said cell in a suitable vector in an orientation relative to a promoter(s) capable of initiating transcription of said cDNA or DNA to double-stranded (ds) RNA upon binding of an appropriate transcription factor to said promoter(s), (b) introducing said library into one or more of said cells comprising said transcription factor, and (c) identifying and isolating a particular **phenotype** of said cell comprising said library and identifying the DNA or cDNA fragment from said library responsible for conferring said **phenotype**. Using this technique it is also possible to assign function to a known DNA sequence by (a) identifying a homolog(s) of said DNA sequence in a cell, (b) isolating the relevant DNA homolog(s) or a fragment thereof from said cell, (c) cloning said homolog or fragment thereof into an appropriate vector in an orientation relative to a suitable promoter(s) capable of initiating transcription of dsRNA from said DNA homolog or fragment upon binding of an appropriate transcription factor to said promoter(s), and (d) introducing said vector into said cell from step (a) comprising said transcription factor. Thus, an ordered library for inhibitory dsRNA technol. can be prepd. harboring every gene of the Caenorhabditis elegans genome; the resulting **phenotypes** can give a functional description to the gene or gene family or gene homologs of the **C. elegans** genome.
Plasmid vectors are described incorporating phage T3, T7, and SP6 RNA polymerase genes and promoters for expression in **C. elegans**. Inhibitory dsRNA technol. can also be used to validate clones identified in yeast 2-hybrid vector expts.

L2 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:300425 CAPLUS
DOCUMENT NUMBER: 131:126184
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in Caenorhabditis briggsae
AUTHOR(S): Vatcher, G. P.; Barbazuk, W. B.; O'Neil, N. J.; Marra, M. A.; Ha, T.; Baillie, D. L.
CORPORATE SOURCE: Institute of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.
SOURCE: Gene (1999), 230(2), 137-144
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In the nematode Caenorhabditis elegans, the maternal effect lethal gene mel-32 encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, mel-32(SHMT) genomic DNA from **C. elegans** was used to screen a **genomic library** from the closely related nematode Caenorhabditis briggsae. The C. briggsae genomic clone identified fully rescues the Mel-32 **phenotype** in **C. elegans**, indicating functional and regulatory conservation. Computer anal. reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved noncoding regions upstream and downstream of the mel-32(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.
REFERENCE COUNT: 38
REFERENCE(S): (1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) de Bono, M; Genetics 1996, V144, P587 CAPLUS
(4) Emmons, S; Proc Natl Acad Sci USA 1979, V76, P1333 CAPLUS
(5) Garrow, T; J Biol Chem 1993, V268, P11910 CAPLUS
(6) Gilleard, J; Gene 1997, V193, P181 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:367026 CAPLUS
DOCUMENT NUMBER: 125:50470
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N-acetylglucosamine transporter from Kluyveromyces lactis
AUTHOR(S): Abeijon, Claudia; Robbins, Phillips W.; Hirschberg, Carlos B.
CORPORATE SOURCE: Dep. Biochem. Mol. Biol., Univ. Massachusetts Med. Cent., Worcester, MA, 01655, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1996), 93(12), 5963-5968
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The mannan chains of Kluyveromyces lactis mannoproteins are similar to those of Saccharomyces cerevisiae except that they lack mannose phosphate and have terminal .alpha.1.fwdarw.2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the human of the Golgi app., by analogy to S. cerevisiae. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of K. lactis, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the K. lactis Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type K. lactis in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid contg. this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homol. to predicted proteins from S. cerevisiae and **C. elegans**. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the golgi UDP-GlcNAc transporter of K. lactis.

L2 ANSWER 8 OF 11 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 1999149080 EMBASE
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in Caenorhabditis briggsae.
AUTHOR: Vatcher G.P.; Barbazuk W.B.; O'Neil N.J.; Marra M.A.; Ha T.; Baillie D.L.
CORPORATE SOURCE: D.L. Baillie, Inst. of Molec. Biology/Biochemistry, Simon Fraser University, Burnaby, BC V5A 1S6, Canada
SOURCE: Gene, (16 Apr 1999) 230/2 (137-144).
Refs: 38
ISSN: 0378-1119 CODEN: GENED6
PUBLISHER IDENT.: S 0378-1119(99)00076-1
COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB In the nematode Caenorhabditis elegans, the maternal effect lethal gene mel-32 encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, mel-32(SHMT) genomic DNA from **C. elegans** was used to screen a **genomic library** from the closely related nematode Caenorhabditis briggsae. The C. briggsae genomic clone identified fully rescues the Mel-32 **phenotype** in **C. elegans**, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL- 32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved non-coding regions upstream and downstream of the mel-32(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors.

L2 ANSWER 9 OF 11 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 96188142 EMBASE
DOCUMENT NUMBER: 1996188142
TITLE: Molecular cloning of the Golgi apparatus uridine diphosphate-N- acetylglucosamine transporter from Kluyveromyces lactis.
AUTHOR: Abeijon C.; Robbins P.W.; Hirschberg C.B.
CORPORATE SOURCE: Biochemistry/Molecular Biology Dept., Massachusetts Univ. Medical Center,Worcester, MA 01655, United States
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) 93/12 (5963-5968). ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English
AB The mannan chains of Klyveromyces lactis mannoproteins are similar to those of Saccharomyces cerevisiae except that they lack mannose phosphate and have terminal .alpha.1.fwdarw.2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to S. cerevisiae. The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of K. lactis, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP- GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the K. lactis Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation. The mnn2-2 mutant was transformed with a **genomic library** from wild-type K. lactis in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter. A 2.4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**. Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred. The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids. The protein contains a leucine zipper motif and has high homology to predicted proteins from S. cerevisiae and **C. elegans**. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc transporter of K. lactis.

L2 ANSWER 10 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)

ACCESSION NUMBER: 1999:343249 SCISEARCH
THE GENUINE ARTICLE: 190LA
TITLE: Identification and characterization of a serine hydroxymethyltransferase isoform in Caenorhabditis briggsae
AUTHOR: Vatcher G P; Barbazuk W B; ONeil N J; Marra M A; Ha T; Baillie D L (Reprint)
CORPORATE SOURCE: SIMON FRASER UNIV, INST MOL BIOL & BIOCHEM, BURNABY, BC V5A 1S6, CANADA (Reprint); SIMON FRASER UNIV, INST MOL BIOL & BIOCHEM, BURNABY, BC V5A 1S6, CANADA; WASHINGTON UNIV, SCH MED, GENOME SEQUENCING CTR, ST LOUIS, MO 63108
COUNTRY OF AUTHOR: CANADA; USA
SOURCE: GENE, (16 APR 1999) Vol. 230, No. 2, pp. 137-144. Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS. ISSN: 0378-1119.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 38

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In the nematode Caenorhabditis elegans, the maternal effect lethal gene mel-32 encodes a serine hydroxymethyltransferase isoform. Since interspecies DNA comparison is a valuable tool for identifying sequences that have been conserved because of their functional importance or role in regulating gene activity, mel-32(SHMT) genomic DNA from **C. elegans** was used to screen a **genomic library** from the closely related nematode Caenorhabditis briggsae. The C. briggsae genomic clone identified fully rescues the Mel-32 **phenotype** in **C. elegans**, indicating functional and regulatory conservation. Computer analysis reveals that CbMEL-32(SHMT) is 92% identical (97% similar) to CeMEL-32(SHMT) at the amino acid level over the entire length of the protein (484 amino acids), whereas the coding DNA is 82.5% identical (over 1455 nucleotides). Several highly conserved noncoding regions upstream and downstream of the mel-32(SHMT) gene reveal potential regulatory sites that may bind trans-acting protein factors, (C) 1999 Published by Elsevier Science B.V. All rights reserved.

L2 ANSWER 11 OF 11 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 96:448469 SCISEARCH
THE GENUINE ARTICLE: UQ455
TITLE: MOLECULAR-CLONING OF THE GOLGI-APPARATUS URIDINE DIPHOSPHATE-N-ACETYLGLUCOSAMINE TRANSPORTER FROM KLUYVEROMYCES-LACTIS
AUTHOR: ABEIJON C (Reprint); ROBBINS P W; HIRSCHBERG C B
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COUNTRY OF AUTHOR: USA
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ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The mannan chains of Klyveromyces lactis mannoproteins are similar to those of Saccharomyces cerevisiae except that they lack mannose phosphate and have terminal alpha 1-->2-linked N-acetylglucosamine. The biosynthesis of these chains probably occurs in the lumen of the Golgi apparatus, by analogy to S. cerevisiae, The sugar donors, GDP-mannose and UDP-GlcNAc, must first be transported from the cytosol, their site of synthesis, via

specific Golgi membrane transporters into the lumen where they are substrates in the biosynthesis of these mannoproteins. A mutant of K. lactis, mnn2-2, that lacks terminal N-acetylglucosamine in its mannan chains in vivo, has recently been characterized and shown to have a specific defect in transport of UDP-GlcNAc into the lumen of Golgi vesicles in vitro. We have now cloned the gene encoding the K. lactis Golgi membrane UDP-GlcNAc transporter by complementation of the mnn2-2 mutation, The mnn2-2 mutant was transformed with a **genomic library** from wild-type K. lactis in a pKD1-derived vector; transformants were isolated and **phenotypic** correction was monitored following cell surface labeling with fluorescein isothiocyanate conjugated to Griffonia simplicifolia II lectin, which binds terminal N-acetylglucosamine, and a fluorescent activated cell sorter, A 2,4-kb DNA fragment was found to restore the wild-type lectin binding **phenotype**, Upon loss of the plasmid containing this fragment, reversion to the mutant **phenotype** occurred, The above fragment contained an open reading frame for a multitransmembrane spanning protein of 328 amino acids, The protein contains a leucine zipper motif and has high homology to predicted proteins from S, cerevisiae and **C. elegans**. In an assay in vitro, Golgi vesicles isolated from the transformant had regained their ability to transport UDP-GlcNAc. Taken together, the above results strongly suggest that the cloned gene encodes the Golgi UDP-GlcNAc trans porter of K. lactis.